

B. AMENDMENTS TO THE SPECIFICATION

Replace the sequence listing currently on file, in both paper and computer readable form, with the attached. The undersigned hereby declares that, to the best of his knowledge, the attached paper copy and computer readable form of same are identical to each other and to information set forth in the application as filed. No new matter is believed presented.

Page 12, lines 5-11:

E2
Cloning and sequencing of the products of RACE PCR showed that the variant sequence of SEQ ID NO: 4 was 5' to SEQ ID NO: 5, and that full length cDNA for the variant SEQ ID NO: 3 contained an additional exon 609 nucleotides long, positioned between SEQ ID NO: 3 and the shared, 3' sequence referred to supra. This exon did not include an ORF. The first available initiation site would be an initial methionine at amino acid 70 of SEQ ID NO: 1. Thus, if expressed, SEQ ID NO: 3 would correspond to a molecule with a 681 base pair, untranslated 5' end and a region encoding 210 amino acids. This is SEQ ID NO: 6. See SEQ ID NO: 6.

Page 13, lines 8-12:

E3
The R11 cDNA library described supra was then screened using SEQ ID NO: 1 and standard methodologies. A 593 base pair cDNA was identified, which was different from any sequences in the data banks consulted. The sequence of this cDNA is set out at included in SEQ ID NO: 8.